

ASBMT BEST ABSTRACT AWARDS FOR BASIC SCIENCE

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Identification of Intestinal Commensal Bacteria Protective Against GVHD in Mice and Humans

Robert Jenq¹, Marcel R.M. van den Brink², ¹Medicine, Memorial Sloan-Kettering Cancer Center, New York, NY; ²Department of Medicine, Memorial Sloan-Kettering Cancer Center, New York, NY

For patients with hematologic malignancies such as leukemias, lymphomas and other related cancers, allogeneic blood/marrow transplantation (allo BMT) is a critically important therapy that can produce cures when chemotherapy alone cannot. More than 25,000 patients undergo allo BMT world-wide each year. A major risk of allo BMT continues to be graft-versus-host disease (GVHD), which results from the donor immune system recognizing the transplant recipient's organs as foreign, leading to life-threatening inflammation. Developing strategies that reduce GVHD but leave global immune function intact should produce a major benefit for patients.

One promising approach that we have developed is targeting the complex community of microbes that reside within our intestinal tracts, collectively termed the intestinal microbiota.

While a relationship between the microbiota and GVHD has been suspected for many years, it remains imperfectly understood. Gut decontamination with antibiotics is practiced at some but not all centers, and there is no consensus regarding ideal choice of antibiotic coverage.

Here we present results demonstrating that the abundance of bacteria belonging to the genus *Blautia*, a commensal commonly found in the intestinal tract of humans, predicts for protection from life-threatening GVHD in allo BMT patients (Figure 1). Furthermore, in murine models, introducing a species of *Blautia* of murine origin reduces GVHD severity (Figure 2A). It appears to do so by inducing regulatory T cells with generation of short-chain fatty acid metabolic byproducts (Figures 2B and 2C).

Additional studies characterizing the natural history of *Blautia* abundance in allo BMT recipients demonstrate that the vast majority of patients begin with abundant amounts of endogenous *Blautia*, but many lose their *Blautia* in a dramatic fashion during the transplantation process (Figure 3A). Interestingly, loss of *Blautia* correlates strongly with reductions in oral nutritional intake in both humans and mice (Figures 3B and 3C). Thus development of nutritional intervention strategies to support *Blautia* abundance following allo BMT could potentially mitigate GVHD. In murine models we have found that these nutritional approaches can successfully prevent loss of *Blautia* as well as reduce severity GVHD.

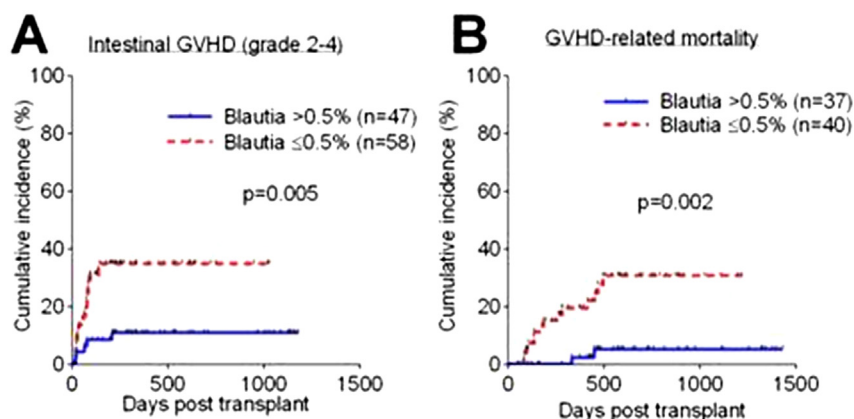


Figure 1. Intestinal *Blautia* abundance predicts for GVHD in humans, A) A cohort of 105 patients, stratified by abundance of *Blautia*, was evaluated for incidence of intestinal GVHD, B) The same cohort stratified by *Blautia* abundance was evaluated for GVHD-related mortality.

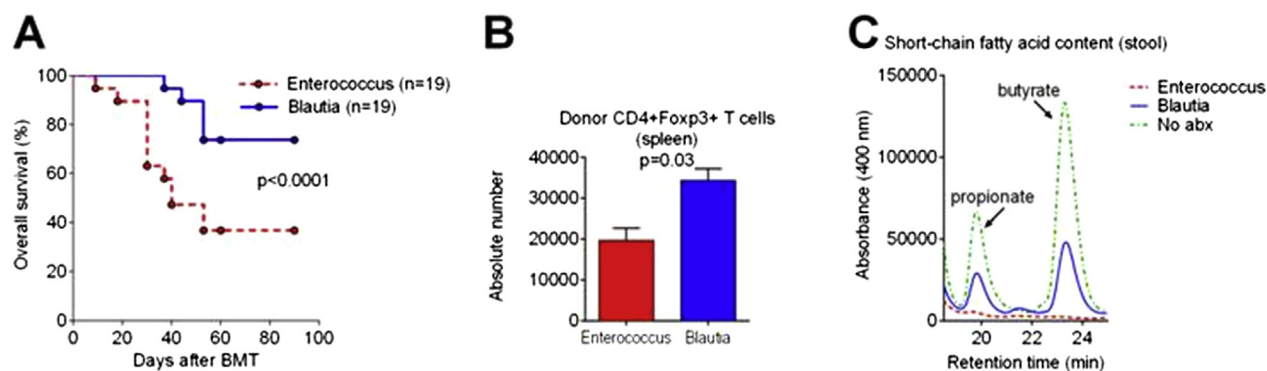


Figure 2. Administration of *Blautia* to mice mitigates GVHD severity. A) B6 mice were treated orally with a 2 day course of vancomycin, a 2 day course of ampicillin, then inoculated 5 and 7 days later with *Blautia* or *Enterococcus* of murine origin, and then 2 weeks later irradiated and transplanted with B10.BR bone marrow and T cells. Presented is overall survival, combined results from 2 experiments. B) Mice were treated as in A. Flow cytometric evaluation of T cell populations, results of a single experiment, mice harvested on BMT day 14 n=4/group. C) Mice were treated with antibiotics and bacteria as in A but without BMT, and stool was evaluated for short chain fatty acid content by HPLC two weeks after bacterial introduction.

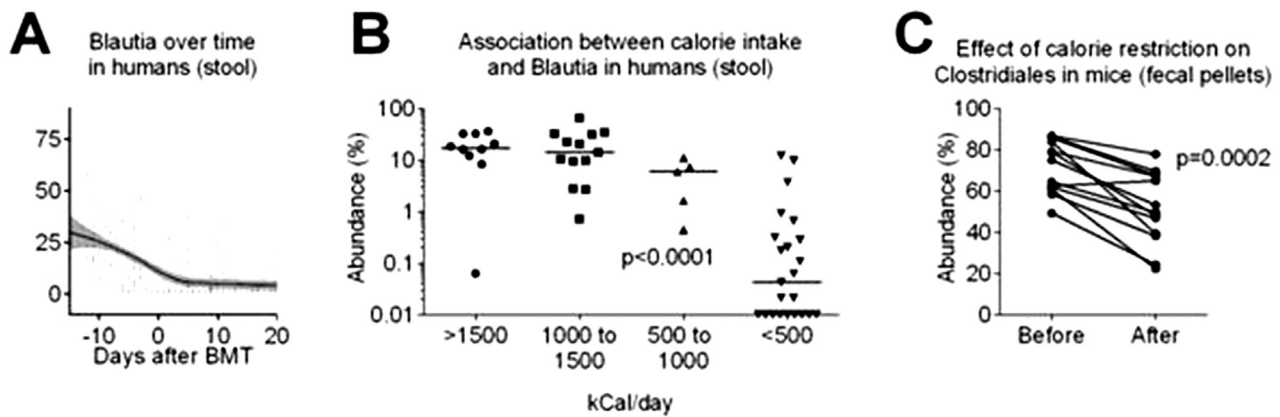


Figure 3. Reduced nutritional intake appears to drive loss of *Blautia* in allo BMT recipients. A) Ninety-four allo BMT patients were evaluated weekly for changes in the intestinal microbiota during transplant hospitalization. *Blautia* abundance is depicted by a solid black line with 95% confidence bands shown in gray constructed using moving average filtering. B) Daily nutritional and microbiota analysis was collected in 5 allo BMT patients during transplant hospitalization, and abundance of *Blautia* analyzed for stool samples stratified by kCal consumption. C) Stool abundance of Clostridiales (the order to which *Blautia* belongs) was assayed in mice before and after one week of 25% reduction in food consumption.

Our results have identified the microbiota as a potent therapeutic target that can be recruited to significantly reduce GVHD. Approaches to potentially translate these findings include investigating the safety of introduction of *Blautia* to allo BMT recipients, or alternatively developing nutritional strategies to support endogenous *Blautia* during the transplantation process.

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CD4⁺ Invariant Natural Killer T Cells Protect from Acute Graft-Versus-Host Disease Lethality through a Dramatic Expansion of Donor-Derived CD4⁺FoxP3⁺ Regulatory T Cells

Dominik Schneidawind¹, Antonio Pierini¹, Maite Alvarez¹, Yuqiong Pan¹, Jeanette Baker¹, Byung Su Kim¹, Hidekazu Nishikii¹, Corina Büchele², Everett Meyer³, Robert Negrin³. ¹Division of Blood and Marrow Transplantation, Department of Medicine, Stanford University, Stanford, CA; ²Department of Pathology, Stanford University, Stanford, CA; ³Division of Blood and Marrow Transplantation, Stanford University Medical Center, Stanford, CA

Invariant natural killer T (iNKT) cells are a rare but potent immunomodulatory subset of lymphocytes in humans (TCR α V α 24-J α 18) and mice (TCR α V α 14-J α 18). It has been shown previously that host iNKT cells require interaction with CD4⁺FoxP3⁺ regulatory T cells to protect from acute GVHD after conditioning with total lymphoid irradiation and anti-thymocyte globulin (Pillai et al., Blood 2009). In this study, we investigated the role of highly purified adoptively transferred donor-derived CD4⁺ iNKT cells in the setting of myeloablative conditioning. Balb/c (H-2Kd) recipient mice were irradiated with 8 Gy and transplanted with T cell-depleted bone marrow together with 1x10⁶ CD4/CD8 T lymphocytes (Tcon) from C57Bl/6 (H-2Kb) donor mice. Mice co-injected with as low as 5x10⁴ highly purified (>99%) CD4⁺ iNKT cells showed a significant survival benefit compared to mice receiving Tcon alone ($p=0.002$). Consistently, weight and GVHD score improved in mice that received CD4⁺ iNKT cells. Signal intensity derived from expanding luciferase expressing alloreactive Tcon was significantly lower in animals treated with CD4⁺ iNKT cells demonstrating inhibition of proliferation of alloreactive Tcon through CD4⁺ iNKT cells ($p<0.0001$). In vivo CFSE proliferation assay confirmed decreased Tcon proliferation in peripheral lymph nodes ($p<0.0001$), mesenteric lymph nodes ($p=0.03$) and spleen ($p=0.0005$). In addition, Tcon from CD4⁺ iNKT cell treated mice showed a significantly lower

expression of activation markers CD44 and CD25. Interestingly, animals treated with CD4⁺ iNKT cells showed a robust expansion of donor-derived Neuropilin-1^{-low}CD4⁺FoxP3⁺ T cells in peripheral lymph nodes, mesenteric lymph nodes, spleen, gut, liver and skin. Moreover, CD4⁺ iNKT cells derived from NKG2D^{-/-} animals were significantly less effective in preventing acute GVHD lethality (WT vs. NKG2D^{-/-} $p=0.003$). Co-injection of CD4⁺ iNKT cells did not abrogate GVL reactions of Tcon towards BCL₁ cells measured by bioluminescence imaging ($p=ns$). With α -GalCer and IL-2 in vitro expanded CD4⁺ iNKT cells had the same protective effect from lethal acute GVHD compared to freshly isolated CD4⁺ iNKT cells ($p=ns$). We conclude that low numbers of highly purified CD4⁺ iNKT cells protect from lethal acute GVHD in mice through a dramatic expansion of donor-derived CD4⁺FoxP3⁺ regulatory T cells with retained GVL effect. Despite the fact that iNKT cells are a rare cell population, the feasibility of in vitro expansion with retained functionality of CD4⁺ iNKT cells provide the basis for clinical translation.

EM and RN contributed equally to this study.

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ATG16L1 Prevents Lethal T-Cell Alloreactivity Mediated By Dendritic Cells

Yusuke Shono¹, Vanessa Hubbard-Lucey², Katie Maurer², Anne Mary Dickinson³, Ernst Holler⁴, Kenneth H. Cadwell², Marcel R.M. van den Brink⁵. ¹Department of Immunology, Memorial Sloan-Kettering Cancer Center, New York, NY; ²Skirball Institute, New York University School of Medicine, New York, NY; ³Institute of Cellular Medicine, Newcastle, United Kingdom; ⁴Haematology/Oncology, University of Regensburg Medical Center, Regensburg, Germany; ⁵Department of Medicine, Memorial Sloan-Kettering Cancer Center, New York, NY

The role of autophagy in GVHD is unknown. We used a MHC-disparate allo-HSCT model (B10.BR into B6) and compared wild-type (WT) vs ATG16L1^{HM} (hypomorphic (HM) for expression of the ATG16L1 protein) recipients. HM recipients developed significantly increased GVHD mortality (Figure A, $P < 0.001$) and morbidity. This was associated with significantly increased levels of inflammatory cytokines, including TNF- α and IL-12 ($P < 0.05$). CFSE analysis demonstrated significantly increased proliferation and activation of alloreactive donor T cells in HM recipients. Alloreactive donor T cells in HM recipients expressed higher levels of LPAM-1,